

RESULT 1

AAB51244

ID AAB51244 standard; protein; 662 AA.

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AC AAB51244;

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DT 26-MAR-2001 (first entry)

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DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.

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KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;

KW immunoregulation; haematopoietic cell regulation; transmembrane;

KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;

KW metal allergy; pollen allergy.

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OS Homo sapiens.

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PN WO200075314-A1.

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PD 14-DEC-2000.

XX

PF 01-JUN-2000; 2000WO-JP003556.

XX

PR 02-JUN-1999; 99JP-00155797.

PR 30-JUL-1999; 99JP-00217797.

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PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

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PI Maeda M, Yaguchi N;

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DR WPI; 2001-061720/07.

DR N-PSDB; AAC92350.

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PT Hematopoietin receptor protein NR10 for screening potential ligands for

PT treatment of immune and hematopoietic disorders such as autoimmune

PT diseases and allergies.

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PS Claim 1; Fig 13-14; 127pp; Japanese.

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CC The present sequence represents a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell regulation
 CC in vivo, and is useful in searching for haematopoietic factors capable of
 CC binding to the receptor. NR10 can be used for the identification of
 CC substances for the treatment and prevention of immune and haematopoietic
 CC disorders including autoimmune diseases and allergies such as metal and
 CC pollen allergy

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SQ Sequence 662 AA;

Query Match 100.0%; Score 3528; DB 4; Length 662;
 Best Local Similarity 100.0%; Pred. No. 6.5e-291;
 Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLSPQPCVNLGMMWTWALWMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKE 60

Db 1 MKLSPQPCVNLGMMWTWALWMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKE 60

Qy 61 TSYTQYTVKRTYAFGEKHDNCTNSSTSENASCSSFFLPRITIPDNYTIEVEAENG DGVI 120

Db 61 TSYTQYTVKRTYAFGEKHDNCTNSSTSENASCSSFFLPRITIPDNYTIEVEAENG DGVI 120

Qy 121 KSHMTYWRLENIakteppkIFRVKPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNS 180

Db 121 KSHMTYWRLENIakteppkIFRVKPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNS 180

Qy 181 TSWMEVNFakNRKDKNQTYNLTGLQPFTEYVIALRCavKESKFWSDSQEKMGMTTEEAP 240

Db 181 TSWMEVNFakNRKDKNQTYNLTGLQPFTEYVIALRCavKESKFWSDSQEKMGMTTEEAP 240

Qy 241 CGLELWRVLKPAEADGRRPVRLLWKKARGAPVLEKTLGYNiWYYPESNTNLtETMNTNQ 300

Db 241 CGLELWRVLKPAEADGRRPVRLLWKKARGAPVLEKTLGYNiWYYPESNTNLtETMNTNQ 300

Qy 301 QLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQCIevMQACVAEDQLVVKWQS 360

Db 301 QLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQCIevMQACVAEDQLVVKWQS 360

Sequence Query
 Appendix A

Sequence Appendix A

Qy 361 SALDVNTWMIEWFPDSDSEPTTSLWESVSQATNWTIQQDKLPFWCYNISVYPMHDKVG 420
Db 361 SALDVNTWMIEWFPDSDSEPTTSLWESVSQATNWTIQQDKLPFWCYNISVYPMHDKVG 420

Qy 421 EPYSIQAYAKEGVPSEGPETKVENIGVKTVTITWKEIPKSERKGIICNYTIFYQAEKGK 480
Db 421 EPYSIQAYAKEGVPSEGPETKVENIGVKTVTITWKEIPKSERKGIICNYTIFYQAEKGK 480

Qy 481 FSKTVNSSILQYGLESKRKTSYIVQVMASTAGGTNGTSINFKTLFSVFEIILITSLI 540
Db 481 FSKTVNSSILQYGLESKRKTSYIVQVMASTAGGTNGTSINFKTLFSVFEIILITSLI 540

Qy 541 GGGLLILILITVAYGLKKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVN 600
Db 541 GGGLLILILITVAYGLKKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVN 600

Qy 601 TEDRILKPCSTPSDKLVIDKLNVNFGNVLQEIFTDEARTQENNLGGEKNGTRILSSCPT 660
Db 601 TEDRILKPCSTPSDKLVIDKLNVNFGNVLQEIFTDEARTQENNLGGEKNGTRILSSCPT 660

Qy 661 SI 662
Db 661 SI 662

